



SEQUENCE LISTING

<110> Oppmann, Birgit
De Waal Malefyt, Rene
Rennick, Donna M.
Kastelein, Robert A.
Wiekowski, Maria T.
Lira, Sergio A.
Narula, Satwant K.

<120> Mammalian Genes; Related Reagents and
Methods

<130> 16622-005001/ DX01042X

<140> US 09/658,699

<141> 2000-09-08

<150> US 60/164,616

<151> 1999-11-10

<150> US 60/153,281

<151> 1999-09-09

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<213> Unknown Organism

<220>

<223> Description of Unknown Organism: surmised Homo
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<220>

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gct	cag	ggc	aga	gct	gtg	cct	ggg	ggc	agc	agc	cct	gcc	tgg	act	cag	96
Ala	Gln	Gly	Arg	Ala	Val	Pro	Gly	Gly	Ser	Ser	Pro	Ala	Trp	Thr	Gln	
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tgc	cag	cag	ctt	tca	cag	aag	ctc	tgc	aca	ctg	gcc	tgg	agt	gca	cat	144
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Cys	Gln	Gln	Leu	Ser	Gln	Lys	Leu	Cys	Thr	Leu	Ala	Trp	Ser	Ala	His		
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cca	cta	gtg	gga	cac	atg	gat	cta	aga	gaa	gag	gga	gat	gaa	gag	act	192	
Pro	Leu	Val	Gly	His	Met	Asp	Leu	Arg	Glu	Glu	Gly	Asp	Glu	Glu	Thr		
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aca	aat	gat	gtt	ccc	cat	atc	cag	tgt	gga	gat	ggc	tgt	gac	ccc	caa	240	
Thr	Asn	Asp	Val	Pro	His	Ile	Gln	Cys	Gly	Asp	Gly	Cys	Asp	Pro	Gln		
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gga	ctc	agg	gac	aac	agt	cag	ttc	tgc	ttg	caa	agg	atc	cac	cag	ggg	288	
Gly	Leu	Arg	Asp	Asn	Ser	Gln	Phe	Cys	Leu	Gln	Arg	Ile	His	Gln	Gly		
	60				65				70					75			
ctg	att	ttt	tat	gag	aag	ctg	cta	gga	tcg	gat	att	ttc	aca	ggg	gag	336	
Leu	Ile	Phe	Tyr	Glu	Lys	Leu	Leu	Gly	Ser	Asp	Ile	Phe	Thr	Gly	Glu		
				80					85					90			
cct	tct	ctg	ctc	cct	gat	agc	cct	gtg	gcg	cag	ctt	cat	gcc	tcc	cta	384	
Pro	Ser	Leu	Leu	Pro	Asp	Ser	Pro	Val	Ala	Gln	Leu	His	Ala	Ser	Leu		
			95					100					105				
ctg	ggc	ctc	agc	caa	ctc	ctg	cag	cct	gag	ggg	cac	cac	tgg	gag	act	432	
Leu	Gly	Leu	Ser	Gln	Leu	Leu	Gln	Pro	Glu	Gly	His	His	Trp	Glu	Thr		
	110					115						120					
cag	cag	att	cca	agc	ctc	agt	ccc	agc	cag	cca	tgg	cag	cgt	ctc	ctt	480	
Gln	Gln	Ile	Pro	Ser	Leu	Ser	Pro	Ser	Gln	Pro	Trp	Gln	Arg	Leu	Leu		
	125					130				135							
ctc	cgc	ttc	aaa	atc	ctt	cgc	agc	ctc	cag	gcc	ttt	gtg	gct	gta	gcc	528	
Leu	Arg	Phe	Lys	Ile	Leu	Arg	Ser	Leu	Gln	Ala	Phe	Val	Ala	Val	Ala		
	140				145				150					155			
gcc	cgg	gtc	ttt	gcc	cat	gga	gca	gca	acc	ctg	agt	ccc	taa			570	
Ala	Arg	Val	Phe	Ala	His	Gly	Ala	Ala	Thr	Leu	Ser	Pro					
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<210> 2
 <211> 189
 <212> PRT
 <213> Unknown Organism

<220>
 <223> surmised Homo sapiens

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			15					20					25				

Gly	Leu	Ala	Val	Pro	Arg	Ser	Ser	Ser	Pro	Asp	Trp	Ala	Gln	Cys	Gln		
		-1	1				5					10					
cag	ctc	tct	cgg	aat	ctc	tgc	atg	cta	gcc	tgg	aac	gca	cat	gca	cca	262	
Gln	Leu	Ser	Arg	Asn	Leu	Cys	Met	Leu	Ala	Trp	Asn	Ala	His	Ala	Pro		
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gcg	gga	cat	atg	aat	cta	cta	aga	gaa	gaa	gag	gat	gaa	gag	act	aaa	310	
Ala	Gly	His	Met	Asn	Leu	Leu	Arg	Glu	Glu	Glu	Asp	Glu	Glu	Thr	Lys		
	30				35					40					45		
aat	aat	gtg	ccc	cgt	atc	cag	tgt	gaa	gat	ggt	tgt	gac	cca	caa	gga	358	
Asn	Asn	Val	Pro	Arg	Ile	Gln	Cys	Glu	Asp	Gly	Cys	Asp	Pro	Gln	Gly		
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ctc	aag	gac	aac	agc	cag	ttc	tgc	ttg	caa	agg	atc	cgc	caa	ggt	ctg	406	
Leu	Lys	Asp	Asn	Ser	Gln	Phe	Cys	Leu	Gln	Arg	Ile	Arg	Gln	Gly	Leu		
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gct	ttt	tat	aag	cac	ctg	ctt	gac	tct	gac	atc	ttc	aaa	ggg	gag	cct	454	
Ala	Phe	Tyr	Lys	His	Leu	Leu	Asp	Ser	Asp	Ile	Phe	Lys	Gly	Glu	Pro		
		80					85					90					
gct	cta	ctc	cct	gat	agc	ccc	atg	gag	caa	ctt	cac	acc	tcc	cta	cta	502	
Ala	Leu	Leu	Pro	Asp	Ser	Pro	Met	Glu	Gln	Leu	His	Thr	Ser	Leu	Leu		
	95					100					105						
gga	ctc	agc	caa	ctc	ctc	cag	cca	gag	gat	cac	ccc	cgg	gag	acc	caa	550	
Gly	Leu	Ser	Gln	Leu	Leu	Gln	Pro	Glu	Asp	His	Pro	Arg	Glu	Thr	Gln		
	110				115				120						125		
cag	atg	ccc	agc	ctg	agt	tct	agt	cag	cag	tgg	cag	cgc	ccc	ctt	ctc	598	
Gln	Met	Pro	Ser	Leu	Ser	Ser	Ser	Gln	Gln	Trp	Gln	Arg	Pro	Leu	Leu		
				130					135					140			
cgt	tcc	aag	atc	ctt	cga	agc	ctc	cag	gcc	ttt	ttg	gcc	ata	gct	gcc	646	
Arg	Ser	Lys	Ile	Leu	Arg	Ser	Leu	Gln	Ala	Phe	Leu	Ala	Ile	Ala	Ala		
			145					150					155				
cgg	gtc	ttt	gcc	cac	gga	gca	gca	act	ctg	act	gag	ccc	tta	gtg	cca	694	
Arg	Val	Phe	Ala	His	Gly	Ala	Ala	Thr	Leu	Thr	Glu	Pro	Leu	Val	Pro		
	160					165					170						
aca	gct	taaggatgcc	caggttccca	tggctaccat	gataagacta	atctatcagc										750	
Thr	Ala																
	175																
ccagacatct	accagttaat	taacccatta	ggacttgtgc	tggttctgtt	tcgtttgttt											810	
tgcgtagaagg	gcaaggacac	cattattaaa	gagaaaagaa	acaaacccca	gagcaggcag											870	
ctggctagag	aaaggagctg	gagaagaaga	ataaagtctc	gagcccttgg	ccttggaagc											930	
gggcaagcag	ctgcgtggcc	tgaggggaag	ggggcggtgg	catcgagaaa	ctgtgagaaa											990	
acccagagca	tcagaaaaag	tgagcccagg	ctttggccat	tatctgtaag	aaaaacaaga											1050	

aaaggggaac attatacttt cctgggtggc tcaggggaaat gtgcagatgc acagtactcc 1110
agacagcagc tctgtacctg cctgctctgt ccctcagttc taacagaatc tagtcactaa 1170
gaactaacag gactaccaat acgaactgac aaa 1203

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<212> PRT
<213> Unknown Organism

<220>
<223> surmised Mus sp.

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Thr Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln
-5 -1 1 5 10
Cys Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His
15 20 25
Ala Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu
30 35 40
Thr Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro
45 50 55
Gln Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln
60 65 70 75
Gly Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly
80 85 90
Glu Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser
95 100 105
Leu Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu
110 115 120
Thr Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro
125 130 135
Leu Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile
140 145 150 155
Ala Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu
160 165 170
Val Pro Thr Ala
175

<210> 5

<211> 102
 <212> PRT
 <213> Unknown Organism

<220>

<223> Description of Unknown Organism: surmised Sus sp.

<400> 5

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			20					25					30		
Ser	Val	Gly	Gln	Leu	His	Ala	Ser	Leu	Leu	Gly	Leu	Arg	Gln	Leu	Leu
		35					40					45			
Gln	Pro	Glu	Gly	His	His	Trp	Glu	Thr	Glu	Gln	Thr	Pro	Ser	Pro	Ser
	50					55					60				
Pro	Ser	Gln	Pro	Trp	Gln	Arg	Leu	Leu	Leu	Arg	Leu	Lys	Ile	Leu	Arg
65					70					75					80
Ser	Leu	Gln	Ala	Phe	Val	Ala	Val	Ala	Ala	Arg	Val	Phe	Ala	His	Gly
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Ala	Ala	Thr	Leu	Ser	Gln										
			100												

<210> 6

<211> 306

<212> PRT

<213> Homo sapiens

<400> 6

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Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	Asp	Thr	Pro	Glu
			20					25					30		
Glu	Asp	Gly	Ile	Thr	Trp	Thr	Leu	Asp	Gln	Ser	Ser	Glu	Val	Leu	Gly
		35					40					45			
Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	Glu	Phe	Gly	Asp	Ala	Gly
	50					55					60				
Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	Leu	Ser	His	Ser	Leu	Leu
65					70					75					80
Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Lys
			85						90					95	
Asp	Gln	Lys	Glu	Pro	Lys	Asn	Lys	Thr	Phe	Leu	Arg	Cys	Glu	Ala	Lys
			100					105					110		
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Thr	Ile	Ser	Thr
		115					120					125			
Asp	Leu	Thr	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Ser	Ser	Asp	Pro	Gln
	130					135					140				
Gly	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Gly
145					150					155					160
Asp	Asn	Lys	Glu	Tyr	Glu	Tyr	Ser	Val	Glu	Cys	Gln	Glu	Asp	Ser	Ala

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 <211> 335
 <212> PRT
 <213> Mus musculus

<400> 8
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 Val Ser Pro Leu Met Ala Met Trp Glu Leu Glu Lys Asp Val Tyr Val
 20 25 30
 Val Glu Val Asp Trp Thr Pro Asp Ala Pro Gly Glu Thr Val Asn Leu
 35 40 45
 Thr Cys Asp Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 50 55 60
 Arg His Gly Val Ile Gly Ser Gly Lys Thr Leu Thr Ile Thr Val Lys
 65 70 75 80
 Glu Phe Leu Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Thr
 85 90 95
 Leu Ser His Ser His Leu Leu Leu His Lys Lys Glu Asn Gly Ile Trp
 100 105 110
 Ser Thr Glu Ile Leu Lys Asn Phe Lys Asn Lys Thr Phe Leu Lys Cys
 115 120 125
 Glu Ala Pro Asn Tyr Ser Gly Arg Phe Thr Cys Ser Trp Leu Val Gln
 130 135 140
 Arg Asn Met Asp Leu Lys Phe Asn Ile Lys Ser Ser Ser Ser Ser Pro
 145 150 155 160
 Asp Ser Arg Ala Val Thr Cys Gly Met Ala Ser Leu Ser Ala Glu Lys
 165 170 175
 Val Thr Leu Asp Gln Arg Asp Tyr Glu Lys Tyr Ser Val Ser Cys Gln
 180 185 190
 Glu Asp Val Thr Cys Pro Thr Ala Glu Glu Thr Leu Pro Ile Glu Leu
 195 200 205
 Ala Leu Glu Ala Arg Gln Gln Asn Lys Tyr Glu Asn Tyr Ser Thr Ser
 210 215 220
 Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln
 225 230 235 240
 Met Lys Pro Leu Lys Asn Ser Gln Val Glu Val Ser Trp Glu Tyr Pro
 245 250 255
 Asp Ser Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Lys Phe Phe Val
 260 265 270
 Arg Ile Gln Arg Lys Lys Glu Lys Met Lys Glu Thr Glu Glu Gly Cys
 275 280 285
 Asn Gln Lys Gly Ala Phe Leu Val Glu Lys Thr Ser Thr Glu Val Gln
 290 295 300
 Cys Lys Gly Gly Asn Val Cys Val Gln Ala Gln Asp Arg Tyr Tyr Asn
 305 310 315 320
 Ser Ser Cys Ser Lys Trp Ala Cys Val Pro Cys Arg Val Arg Ser
 325 330 335

<210> 9
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 <212> DNA
 <213> Rattus norvegicus

<400> 9
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gcccctggag	aaacggtgac	cctcacctgt	gacagtcctg	aagaagatga	catcacctgg	180
acctcagacc	agagacgtgg	agtcataggc	tctggaaaga	ccctgaccat	caactgtcaga	240
gagtttctag	atgctggcca	atacacctgc	cacagaggag	gcgagactct	gagccactca	300
catctgctgc	tccacaagaa	ggaaaatgga	atttggtcca	ccgagatttt	aaaaaatttc	360
aaaaataaga	ctttcctgaa	gtgtgaagca	ccaaactact	ccggacgggt	cacctgctca	420
tggctcgtgc	acagaaacac	ggacttgaag	tttaacatca	agagcagcag	cagttcccct	480
gagtctcggg	cggtgacatg	tggacgagca	tctctgtctg	cagagaaggt	cacactgaac	540
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gaggagaccc	tgcccattga	actggtgggt	gaggcccagc	agcagaataa	atatgagaac	660
tacagcacca	gcttcttcat	cagggacatc	atcaaaccgg	acccacccaa	gaacctgcag	720
gtgaaacctt	tgaagaactc	tcaggtggag	gtcagctggg	agtaccctga	ctcctggagc	780
actccccatt	cctacttctc	cctcaagttc	ttcgtccgca	tccagcgcaa	gaaagaaaag	840
acgaaggaga	cagaggagga	gtgtaaccag	aaaggtgcgt	tcctcgtaga	gaagacctct	900
gccgaagtcc	aatgcaaagg	ggcgaatatc	tgcgtgcaag	cgcaggaccg	ctactacaat	960
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<210> 10

<211> 335

<212> PRT

<213> Rattus norvegicus

<400> 10

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			20					25					30		
Val	Glu	Val	Asp	Trp	Arg	Pro	Asp	Ala	Pro	Gly	Glu	Thr	Val	Thr	Leu
		35					40					45			
Thr	Cys	Asp	Ser	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln
	50					55					60				
Arg	Arg	Gly	Val	Ile	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Thr	Val	Arg
65					70					75					80
Glu	Phe	Leu	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Arg	Gly	Gly	Glu	Thr
				85					90					95	
Leu	Ser	His	Ser	His	Leu	Leu	Leu	His	Lys	Lys	Glu	Asn	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Glu	Ile	Leu	Lys	Asn	Phe	Lys	Asn	Lys	Thr	Phe	Leu	Lys	Cys
		115					120					125			
Glu	Ala	Pro	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Ser	Trp	Leu	Val	His
	130					135					140				
Arg	Asn	Thr	Asp	Leu	Lys	Phe	Asn	Ile	Lys	Ser	Ser	Ser	Ser	Ser	Pro
145					150					155					160
Glu	Ser	Arg	Ala	Val	Thr	Cys	Gly	Arg	Ala	Ser	Leu	Ser	Ala	Glu	Lys
				165					170					175	
Val	Thr	Leu	Asn	Gln	Arg	Asp	Tyr	Glu	Lys	Tyr	Ser	Val	Ala	Cys	Gln
		180						185					190		
Glu	Asp	Val	Thr	Cys	Pro	Thr	Ala	Glu	Glu	Thr	Leu	Pro	Ile	Glu	Leu
	195						200					205			
Val	Val	Glu	Ala	Gln	Gln	Gln	Asn	Lys	Tyr	Glu	Asn	Tyr	Ser	Thr	Ser
	210					215					220				
Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn	Leu	Gln
225					230					235					240
Val	Lys	Pro	Leu	Lys	Asn	Ser	Gln	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro
				245					250					255	
Asp	Ser	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Lys	Phe	Phe	Val
			260					265					270		

Arg	Ile	Gln	Arg	Lys	Lys	Glu	Lys	Thr	Lys	Glu	Thr	Glu	Glu	Glu	Cys
	275						280					285			
Asn	Gln	Lys	Gly	Ala	Phe	Leu	Val	Glu	Lys	Thr	Ser	Ala	Glu	Val	Gln
	290						295				300				
Cys	Lys	Gly	Ala	Asn	Ile	Cys	Val	Gln	Ala	Gln	Asp	Arg	Tyr	Tyr	Asn
305				310				315							320
Ser	Ser	Cys	Ser	Lys	Trp	Thr	Cys	Val	Pro	Cys	Arg	Gly	Arg	Ser	
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<210> 11
 <211> 821
 <212> DNA
 <213> Rattus norvegicus

<400> 11

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ggactggcgc	cccgatgccc	ctggagaaac	ggtgaccttc	acctgtgaca	gtcctgaaga	180
agatgacatc	acctggacct	cagaccagag	acgtggagtc	ataggctctg	gaaagacctt	240
gaccatcact	gtcagagagt	ttctagatgc	tggccaatac	acctgccaca	gaggaggcga	300
gactctgagc	cactcacatc	tgctgctcca	caagaaggaa	aatggaattt	ggtccaccga	360
gattttaaaa	aattttcaaaa	ataagacttt	cctgaagaga	gaagcaccaa	actactccgg	420
acggttcacc	tgctcatggc	tggtgcacag	aaacacggac	ttgaagttta	acatcaagag	480
cagcagcagt	tcccctgagt	ctcgggcggt	gacatgtgga	gcagcatctc	tgtctgcaga	540
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gaataaatat	gagaactaca	gcaccagctt	cttcatcagg	gacatcatca	aaccggaccc	720
acccaagaac	ctgcaggtga	aacctttgaa	gaactctcag	gtggaggtca	gctgggagta	780
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 <212> PRT
 <213> Rattus norvegicus

<400> 12

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			20					25					30		
Val	Glu	Val	Asp	Trp	Arg	Pro	Asp	Ala	Pro	Gly	Glu	Thr	Val	Thr	Leu
			35				40					45			
Thr	Cys	Asp	Ser	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln
			50			55					60				
Arg	Arg	Gly	Val	Ile	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Thr	Val	Arg
65				70					75					80	
Glu	Phe	Leu	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Arg	Gly	Gly	Glu	Thr
			85						90					95	
Leu	Ser	His	Ser	His	Leu	Leu	Leu	His	Lys	Lys	Glu	Asn	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Glu	Ile	Leu	Lys	Asn	Phe	Lys	Asn	Lys	Thr	Phe	Leu	Lys	Arg
			115				120					125			
Glu	Ala	Pro	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Ser	Trp	Leu	Val	His
			130			135					140				
Arg	Asn	Thr	Asp	Leu	Lys	Phe	Asn	Ile	Lys	Ser	Ser	Ser	Ser	Ser	Pro
145				150					155						160
Glu	Ser	Arg	Ala	Val	Thr	Cys	Gly	Ala	Ala	Ser	Leu	Ser	Ala	Glu	Lys

				165						170						175			
Val	Thr	Leu	Asn	Gln	Arg	Asp	Tyr	Glu	Lys	Tyr	Ser	Val	Ala	Cys	Gln				
			180					185					190						
Glu	Asp	Val	Thr	Cys	Pro	Thr	Ala	Glu	Glu	Thr	Leu	Pro	Ile	Glu	Leu				
		195					200					205							
Val	Val	Glu	Ala	Gln	Gln	Gln	Asn	Lys	Tyr	Glu	Asn	Tyr	Ser	Thr	Ser				
	210					215					220								
Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn	Leu	Gln				
225					230				235					240					
Val	Lys	Pro	Leu	Lys	Asn	Ser	Gln	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro				
			245						250					255					
Asp	Ser	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu								
			260					265											

<210> 13
 <211> 990
 <212> DNA
 <213> Felis catus

<400> 13

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gcccccgag	aaatggtggt	cctcacctgt	gacacgcctg	aagaagatga	catcacctgg	180
acctctgacc	agagcagtga	agtcctaggc	tctggtaaaa	ctctgaccat	ccaagtcaaa	240
gaatttgtag	atgctggcca	gtatacctgt	cataaaggag	gcgagggtct	gagccattcg	300
ttcctcctga	tacacaaaaa	ggaagatgga	atttggtcca	ctgatattct	aaggggaacag	360
aaagaatcca	aaaataagat	ctttctaaaa	tgtgaggcaa	agaattattc	tggacgtttc	420
acctgctggt	ggctgacggc	aatcagtacc	gatttgaaat	tcactgtcaa	aagcagcaga	480
ggctcctctg	accccccaagg	ggtgacttgt	ggagcagcga	cactctcagc	agagaagggtc	540
agagtggaca	acagggatta	taagaagtac	acagtggagt	gtcaggaggg	cagtgcctgc	600
ccggctgccg	aggagagcct	acccattgaa	gtcgtggtgg	acgctattca	caagctcaag	660
tacgaaaaat	acaccagcag	cttcttcac	aggacatca	tcaaaccgga	cccacccaag	720
aacctgcaac	tgaagccatt	aaaaaattct	cggcatgtgg	aagtgagctg	ggaataccct	780
gacacctgga	gcacccca	ttcctacttc	tccttaacat	ttggcgtaga	ggtccagggc	840
aagaacaaca	gagaaaagaa	agacagactc	tccgtggaca	agacctcagc	caaggctcgtg	900
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agcaactggg	catccgtgtc	ctgcagttag				990

<210> 14
 <211> 329
 <212> PRT
 <213> Felis catus

<400> 14

Met	His	Pro	Gln	Gln	Leu	Val	Ile	Ala	Trp	Phe	Ser	Leu	Val	Leu	Leu
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Ala	Pro	Pro	Leu	Met	Ala	Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val
		20					25				30				
Val	Glu	Leu	Asp	Trp	His	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
	35					40					45				
Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln
	50				55					60					
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65				70				75					80		
Glu	Phe	Ala	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
		85					90					95			
Leu	Ser	His	Ser	Phe	Leu	Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp

			100					105					110				
Ser	Thr	Asp	Ile	Leu	Arg	Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe		
		115					120					125					
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp		
		130				135					140						
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg		
145					150					155					160		
Gly	Ser	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser		
			165						170					175			
Ala	Glu	Lys	Val	Arg	Val	Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val		
			180					185					190				
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro		
		195					200					205					
Ile	Glu	Val	Val	Val	Asp	Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr		
	210				215						220						
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys		
225					230					235					240		
Asn	Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser		
				245				250						255			
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu		
			260					265					270				
Thr	Phe	Gly	Val	Gln	Val	Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp		
		275				280					285						
Arg	Leu	Ser	Val	Asp	Lys	Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp		
	290				295						300						
Ala	Lys	Ile	Arg	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp		
305				310					315						320		
Ser	Asn	Trp	Ala	Ser	Val	Ser	Cys	Ser									
				325													

<210> 15

<211> 1006

<212> DNA

<213> Felis catus

<400> 15

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gcccccgag	aaatggtggt	cctcacctgc	aatactctg	aagaagatga	catcacctgg	180
acctctgacc	agagcagtga	agtcctaggc	tctggtaaaa	ctctgaccat	ccaagtcaaa	240
gaatttgtag	atgctggcca	gtatacctgt	cataaaggag	gcgaggttct	gagccattcg	300
ttcctcctga	tacacaaaaa	ggaagatgga	atttggtcca	ctgatatctt	aagggaacag	360
aaagaatcca	aaaataagat	ctttctaaaa	tgtgaggcaa	agaattattc	tggaacgtttc	420
acctgctggt	ggctgacggc	aatcagtagc	gatttgaaat	tactgtcaa	aagcagcaga	480
ggctcctctg	acccccaaaga	ggtgacttgt	ggagcagcga	cactctcagc	agagaaggtc	540
agagtggaca	acagggatta	taagaagtac	acagtggagt	gtcaggaggg	cagtgcctgc	600
ccggctgccg	aggagagcct	acccattgaa	gtcgtggtgg	acgctattca	caagctcaag	660
tacgaaaact	acaccagcag	cttcttcatc	agggacatca	tcaaaccgga	cccacccaag	720
aacctgcaac	tgaagccatt	aaaaaattct	cggcatgtgg	aagtgagctg	ggaataccct	780
gacacctgga	gcacccca	ttcctacttc	tccttaacat	ttggcgtaca	ggtccagggc	840
aagaacaaca	gagaaaagaa	agacagactc	tccgtggaca	agacctcagc	caaggtcgtg	900
tgccacaagg	atgcccaagat	ccgcgtgcaa	gccagagacc	gctactatag	ctcatcctgg	960
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<210> 16

<211> 329

<212> PRT

<213> Felis catus

<400> 16

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Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu
 1          5          10          15
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20          25          30
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35          40          45
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 50          55          60
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65          70          75          80
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85          90          95
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100          105          110
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115          120          125
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130          135          140
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145          150          155          160
Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser
165          170          175
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180          185          190
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195          200          205
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210          215          220
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225          230          235          240
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245          250          255
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260          265          270
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275          280          285
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290          295          300
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305          310          315          320
Ser Asn Trp Ala Ser Val Ser Cys Ser
325

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<210> 17

<211> 1058

<212> DNA

<213> Equus caballus

<400> 17

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gccctgggag aaatgggtgg cctcacctgc aataccctg aagaagaagg catcacctgg      180
acctcgcccc agagcaatga ggtcttaggc tctggcaaaa ccttgaccat ccaagtcaaa      240
gagtttggag atgctggctg gtacacctgt cacaaggag gcgaggttct gagccattct      300

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cacctgctgc	ttcacaagaa	ggaagatgga	atttggtcca	ctgacatttt	aaaagaccag	360
aaagaatcca	aaaataagac	ctttctaaaa	tgtgaggcaa	agaattattc	cggacgtttc	420
acatgctggt	ggctgacagc	aatcagtact	gatttgaaat	tcagtgtcaa	aagcagcaga	480
ggttcctctg	acccccgagg	ggtgacgtgt	ggagcagcga	cactctccgc	agagagggtc	540
agcgtggacg	acagggagta	taagaagtac	acggtggagt	gtcaggaggg	cagtgcctgc	600
ccggccgccg	aggagagcct	gcccattgag	atcgtgggtg	atgctgttca	caagctcaag	660
tatgaaaact	acaccagcgg	cttcttcatc	agggacatca	tcaaaccaga	cccaccaag	720
aacctgcagc	tgaagccatt	aaagaattct	cggcaggtgg	aggtcagctg	ggagtacccc	780
gagacctgga	gcacccca	ttctacttc	tccctgacat	tctctattca	ggtccagggc	840
aagaacaaga	aggaaaggaa	agacagactc	ttcatggatg	agacttcagc	cacagtcaca	900
tgccacaagg	atggccagat	ccgtgtccaa	gccagggacc	gctactacag	ctcatcctgg	960
agcgaatggg	catccgtatc	ctgcagttag	ggatgcagac	tcaggcagcc	caggccagac	1020
ctgaacactc	agtgtaccca	ggttctaacc	tcagtatg			1058

<210> 18

<211> 329

<212> PRT

<213> Equus caballus

<400> 18

Met	Cys	His	Gln	Trp	Leu	Val	Leu	Ser	Trp	Phe	Ser	Leu	Val	Leu	Leu
1				5					10					15	
Ala	Ser	Pro	Leu	Met	Ala	Ile	Trp	Glu	Leu	Glu	Lys	Asp	Val	Tyr	Val
			20					25					30		
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
		35					40					45			
Thr	Cys	Asn	Thr	Pro	Glu	Glu	Gly	Ile	Thr	Trp	Thr	Ser	Ala	Gln	
	50					55				60					
Ser	Asn	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70					75					80
Glu	Phe	Gly	Asp	Ala	Gly	Trp	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
				85					90					95	
Leu	Ser	His	Ser	His	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Thr	Phe
		115					120					125			
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp
		130				135					140				
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg
145					150				155						160
Gly	Ser	Ser	Asp	Pro	Arg	Gly	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser
			165					170						175	
Ala	Glu	Arg	Val	Ser	Val	Asp	Asp	Arg	Glu	Tyr	Lys	Lys	Tyr	Thr	Val
		180					185						190		
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro
		195					200					205			
Ile	Glu	Ile	Val	Val	Asp	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr
	210					215					220				
Thr	Ser	Gly	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys
225					230				235						240
Asn	Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser
			245					250					255		
Trp	Glu	Tyr	Pro	Glu	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu
		260					265						270		
Thr	Phe	Ser	Ile	Gln	Val	Gln	Gly	Lys	Asn	Lys	Lys	Glu	Arg	Lys	Asp
		275				280					285				
Arg	Leu	Phe	Met	Asp	Glu	Thr	Ser	Ala	Thr	Val	Thr	Cys	His	Lys	Asp

290 295 300
 Gly Gln Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320
 Ser Glu Trp Ala Ser Val Ser Cys Ser
 325

<210> 19
 <211> 1399
 <212> DNA
 <213> Homo sapiens

<400> 19
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 aagaaagatg tttatgtcgt agaattggat tggatcccg atgcccctgg agaaatggtg 180
 gtccctcacct gtgacacccc tgaagaagat ggtatcacct ggaccttga ccagagcagt 240
 gaggtcttag gctctggcaa aaccctgacc atccaagtca aagagtgttg agatgctggc 300
 cagtacacct gtcacaaagg aggcgaggtt ctaagccatt cgctcctgct gcttcacaaa 360
 aaggaagatg gaatttggtc cactgatatt ttaaaggacc agaaagaacc caaaaataag 420
 acctttctaa gatgcgaggc caagaattat tctggacgtt tcacctgctg gtggctgacg 480
 acaatcagta ctgatttgac attcagtgtc aaaagcagca gaggtctctt tgacccccaa 540
 ggggtgacgt gcggagctgc taccctctct gcagagagag tcagagggga caacaaggag 600
 tatgagtact cagtggagtg ccaggaggac agtgcctgcc cagctgctga ggagagtctg 660
 cccattgagg tcatggtgga tgccgttcac aagctcaagt atgaaaacta caccagcagc 720
 ttcttcatca gggacatcat caaacctgac ccaccaaga acttgcagct gaagccatta 780
 aagaattctc ggcaggtgga ggtcagctgg gagtaccctg acacctggag tactccacat 840
 tctacttctt ccctgacatt ctgcgttcag gtccagggca agagcaagag agaaaagaaa 900
 gatagagtct tcacggacaa gacctcagcc acggtcatct gccgcaaaaa tgccagcatt 960
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 atgttttaaag acacaacgga atagacccaa aaagataatt tctatctgat ttgctttaaa 1140
 acgttttttt aggatcacia tgatatcttt gctgtatttg tatagttaga tgctaaatgc 1200
 tcattgaaac aatcagctaa tttatgtata gattttccag ctctcaagtt gccatggggc 1260
 ttcatgctat ttaaataattt aagtaattta tgtatttatt agtatattac tgttatttaa 1320
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 agtccctatt atgcaaaat 1399

<210> 20
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 20
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 20 25 30
 Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45
 Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln
 50 55 60
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95
 Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
 100 105 110

Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
 115 120 125
 Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
 145 150 155 160
 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
 165 170 175
 Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
 180 185 190
 Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
 195 200 205
 Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
 210 215 220
 Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
 225 230 235 240
 Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
 245 250 255
 Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
 260 265 270
 Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
 275 280 285
 Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
 290 295 300
 Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
 305 310 315 320
 Glu Trp Ala Ser Val Pro Cys Ser
 325

<210> 21
 <211> 1012
 <212> DNA
 <213> Capra hircus

<400> 21
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 gtcctctggag aaacagtggg cctcacgtgt gacactcctg aagaagacgg catcacctgg 180
 acctcagacc agagcagtga ggtcctgggc tctggcaaaa ccttgaccat ccaagtcaaa 240
 gagtttggag atgctgggca gtacacctgt caciaaggag gcgaggttct gagtcgttca 300
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 aaagaaccca aagctaagag ttttttaaaa tgtgaggcaa aggattattc tggacacttc 420
 acctgctcgt ggctgacagc aatcagtact aatctgaaat tcagtgtcaa aagcagcaga 480
 ggctcctctg acccccgagg ggtgacgtgc ggagcagcgt cactctcagc agagaaggtc 540
 agcatggacc acagggagta taacaagtac acagtggagt gtcaggaggg cagtgcctgc 600
 ccggccgccg aggagagcct gccattgag gtcgtgatgg aagctgtgca caagctcaag 660
 tatgaaaact acaccagcag cttcttcac agggacatca tcaaaccaga cccacccaag 720
 aacctgcaac tgagaccact aaagaattct cggcagggtg aggtcagctg ggagtaccct 780
 gacacgtgga gcacccaca ttcctacttc tccttgacgt tttgtgttca ggtccaggga 840
 aagaacaaga gagaaaagaa actcttcacg gaccaaacct cagccaaagt cacatgccac 900
 aaggatgcc aatccgtgt gcaagcccgg gaccgctact acagctcatt ctggagtcaa 960
 tgggcatctg tgtcctgcag ttaggttcta acctcagtat gaaacctcag ag 1012

<210> 22
 <211> 327
 <212> PRT
 <213> Capra hircus

<400> 22

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Met His Pro Gln Gln Leu Val Val Ser Trp Phe Ser Leu Val Leu Leu
 1          5          10          15
Ala Ser Pro Ile Val Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
          20          25          30
Val Glu Leu Asp Trp Tyr Pro Asn Ala Pro Gly Glu Thr Val Val Leu
          35          40          45
Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Ser Asp Gln
          50          55          60
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65          70          75          80
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
          85          90          95
Leu Ser Arg Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
          100          105          110
Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Ala Lys Ser Phe
          115          120          125
Leu Lys Cys Glu Ala Lys Asp Tyr Ser Gly His Phe Thr Cys Ser Trp
          130          135          140
Leu Thr Ala Ile Ser Thr Asn Leu Lys Phe Ser Val Lys Ser Ser Arg
145          150          155          160
Gly Ser Ser Asp Pro Arg Gly Val Thr Cys Gly Ala Ala Ser Leu Ser
          165          170          175
Ala Glu Lys Val Ser Met Asp His Arg Glu Tyr Asn Lys Tyr Thr Val
          180          185          190
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
          195          200          205
Ile Glu Val Val Met Glu Ala Val His Lys Leu Lys Tyr Glu Asn Tyr
          210          215          220
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225          230          235          240
Asn Leu Gln Leu Arg Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser
          245          250          255
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
          260          265          270
Thr Phe Cys Val Gln Val Gln Gly Lys Asn Lys Arg Glu Lys Lys Leu
          275          280          285
Phe Thr Asp Gln Thr Ser Ala Lys Val Thr Cys His Lys Asp Ala Asn
          290          295          300
Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Phe Trp Ser Glu
305          310          315          320
Trp Ala Ser Val Ser Cys Ser
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<210> 23

<211> 1080

<212> DNA

<213> Macaca mulatta

<400> 23

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tggtaccctgg atgcccctgg agaaatgggt gtcctcacct gtgacacccc tgaagaagat      180
gggtatcacct ggaccttgga ccagagtggg gaggtcttag gctctggcaa aaccctgacc      240
atccaagtca aagagtttgg agatgctggc cagtacacct gtcacaaaagg aggcgaggct      300
ctaagccatt cactcctgct gcttcacaaa aaggaagatg gaatttggtc cactgatgtt      360

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agtgcctgcc	cagccgctga	ggagaggctg	cccattgagg	tcatgggtgga	tgccattcac	660
aagctcaagt	atgaaaacta	caccagcagc	ttcttcatca	gggacatcat	caaaccgcac	720
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gagtaccctg	acacctggag	tactccacat	tcctacttct	ccctgacatt	ctgcatccag	840
gtccagggca	agagcaagag	agaaaagaaa	gatagaatct	tcacagacaa	gacctcagcc	900
acggtcatct	gccgcaaaaa	tgccagcttt	agcgtgcagg	cccaggaccg	ctactatagc	960
tcactttgga	gcgaatgggc	atctgtgccc	tgcagttagg	ttgtgatccc	aggatgaaaa	1020
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<210> 24

<211> 328

<212> PRT

<213> Macaca mulatta

<400> 24

Met	Cys	His	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Phe	Leu
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Ala	Ser	Pro	Leu	Met	Ala	Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val
			20					25					30		
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
		35					40					45			
Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Leu	Asp	Gln
	50					55					60				
Ser	Gly	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70					75					80
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Ala
			85						90					95	
Leu	Ser	His	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Asp	Val	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Asn	Lys	Thr	Phe
		115					120					125			
Leu	Arg	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp
	130					135					140				
Leu	Thr	Thr	Ile	Ser	Thr	Asp	Leu	Thr	Phe	Ser	Val	Lys	Ser	Ser	Arg
145					150					155					160
Gly	Ser	Ser	Asn	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser
			165						170					175	
Ala	Glu	Arg	Val	Arg	Gly	Asp	Asn	Lys	Glu	Tyr	Glu	Tyr	Ser	Val	Glu
			180					185					190		
Cys	Gln	Glu	Asp	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Arg	Leu	Pro	Ile
	195					200						205			
Glu	Val	Met	Val	Asp	Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr
	210					215					220				
Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn
225					230					235					240
Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser	Trp
			245						250					255	
Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr
		260						265					270		
Phe	Cys	Ile	Gln	Val	Gln	Gly	Lys	Ser	Lys	Arg	Glu	Lys	Lys	Asp	Arg
		275					280					285			
Ile	Phe	Thr	Asp	Lys	Thr	Ser	Ala	Thr	Val	Ile	Cys	Arg	Lys	Asn	Ala
	290					295					300				

Ser Phe Ser Val Gln Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
 305 310 315 320
 Glu Trp Ala Ser Val Pro Cys Ser
 325

<210> 25
 <211> 1012
 <212> DNA
 <213> Bos taurus

<400> 25
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 gctcctggag aaacagtggg cctcacatgt gacactcctg aagaagatgg catcacctgg 180
 acctcagacc agagcagtga ggtcttgggc tctggcaaaa ccttgaccat ccaagtcaaa 240
 gagtttggag atgctgggca gtacacctgt cacaaaggag gcgaggctct gagtctgtca 300
 ctctcctcgc tgcacaaaaa ggaagatgga atttggtcca ctgatatttt aaaggatcag 360
 aaagaaccca aagctaagag ttttttaaaa tgtgaggcaa aggattattc tggacacttc 420
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 ggctcctctg acccccaggg ggtgacgtgc ggagcagcgt tgctctcagc agagaaggtc 540
 agcttggagc acagggagta taacaagtac acagtggagt gtcaggaggg cagcgcctgc 600
 ccagccgctg aggagagcct gcttattgag gtcgtggtag aagctgtgca caagctcaag 660
 tatgaaaact acaccagcag cttcttcacg agggacatca tcaaaccaga cccaccaag 720
 aacctgcaac tgagaccatt aaagaattct cggcaggtgg aggtcagctg ggagtaccct 780
 gacacgtgga gcaccccgca ttcctacttc tccctgacgt tttgtgttca ggtccaggga 840
 aagaacaaga gagaaaagaa actcttcacg gaccaaact cagccaaagt cacatgccac 900
 aaggatgcca acgtccgcgt gcaagcccg gaccgctact acagctcatt ctggagtga 960
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<210> 26
 <211> 327
 <212> PRT
 <213> Bos taurus

<400> 26
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 20 25 30
 Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Thr Val Val Leu
 35 40 45
 Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Ser Asp Gln
 50 55 60
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Ala
 85 90 95
 Leu Ser Arg Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Ala Lys Ser Phe
 115 120 125
 Leu Lys Cys Glu Ala Lys Asp Tyr Ser Gly His Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
 145 150 155 160
 Gly Ser Ser Asp Pro Arg Gly Val Thr Cys Gly Ala Ala Leu Leu Ser
 165 170 175

Ala	Glu	Lys	Val	Ser	Leu	Glu	His	Arg	Glu	Tyr	Asn	Lys	Tyr	Thr	Val
			180					185					190		
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Leu
		195					200					205			
Ile	Glu	Val	Val	Val	Glu	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr
	210					215					220				
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys
225					230					235					240
Asn	Leu	Gln	Leu	Arg	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser
			245						250				255		
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu
		260						265					270		
Thr	Phe	Cys	Val	Gln	Val	Gln	Gly	Lys	Asn	Lys	Arg	Glu	Lys	Lys	Leu
		275					280					285			
Phe	Met	Asp	Gln	Thr	Ser	Ala	Lys	Val	Thr	Cys	His	Lys	Asp	Ala	Asn
	290					295					300				
Val	Arg	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Phe	Trp	Ser	Glu
305					310					315					320
Trp	Ala	Ser	Val	Ser	Cys	Ser									
				325											

<210> 27

<211> 993

<212> DNA

<213> Cervus elaphus

<400> 27

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gctcctggag	aaacggtggt	cctcaggtgt	gacactcctg	aagaagacgg	tatcacctgg	180
acctcagacc	agagcagtga	ggtcttgggc	tctggcaaaa	ccttgaccgt	ccaagtcaaa	240
gagtttgag	atgctgggca	gtacacctgt	cacaaaggag	gcgaggttct	gagtcgttca	300
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aaagaaccca	aagccaagag	ttttttaaaa	tgtgaggcaa	aggattattc	tggacacttc	420
acctgctggt	ggctgacagc	aatcagtagt	gatttgaaat	tcagtgtcaa	aagcagcaga	480
ggctcctctg	acccccgagg	ggtgacgtgc	ggagcagcgt	cgctctcaac	agagaagggtc	540
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ccggccgccc	aggagagcct	gcccattgag	gtcgtagtgg	aagctgtgca	caagctcaag	660
tatgaaaact	acaccagcag	cttcttcac	agggacatca	tcaaaccaga	cccacccaag	720
aacctgcaac	tgagaccatt	aaagaattct	cggcaggtgg	aggtcagctg	ggagtaccct	780
gacacgtgga	gcaccccaca	ttcctacttc	tccctgacgt	tttgtgttca	gggccaggga	840
aagaacaaga	gagaaaagaa	actcttcac	gaccaaact	cagccaaagt	cacgtgtcac	900
aaggatgcc	gcatccgct	gcaagcccgg	gaccgctact	acaactcatt	ctggagtga	960
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<210> 28

<211> 327

<212> PRT

<213> Cervus elaphus

<400> 28

Met	His	Pro	Gln	Gln	Leu	Val	Val	Ser	Trp	Phe	Ser	Leu	Val	Leu	Leu
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Thr	Ser	Pro	Ile	Val	Ala	Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val
		20					25					30			
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Thr	Val	Val	Leu
	35						40					45			

Arg	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Ser	Asp	Gln
50						55					60				
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Val	Gln	Val	Lys
65					70					75					80
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
				85					90					95	
Leu	Ser	Arg	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Ala	Lys	Ser	Phe
		115					120					125			
Leu	Lys	Cys	Glu	Ala	Lys	Asp	Tyr	Ser	Gly	His	Phe	Thr	Cys	Trp	Trp
	130					135					140				
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg
145					150				155						160
Gly	Ser	Ser	Asp	Pro	Arg	Gly	Val	Thr	Cys	Gly	Ala	Ala	Ser	Leu	Ser
				165					170					175	
Thr	Glu	Lys	Val	Ile	Val	Asp	His	Arg	Glu	Tyr	Lys	Lys	Tyr	Thr	Val
			180					185					190		
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro
		195					200				205				
Ile	Glu	Val	Val	Val	Glu	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr
	210					215					220				
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys
225					230					235					240
Asn	Leu	Gln	Leu	Arg	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser
				245				250						255	
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu
			260					265					270		
Thr	Phe	Cys	Val	Gln	Val	Gln	Gly	Lys	Asn	Lys	Arg	Glu	Lys	Lys	Leu
		275					280					285			
Phe	Met	Asp	Gln	Thr	Ser	Ala	Lys	Val	Thr	Cys	His	Lys	Asp	Ala	Ser
	290					295					300				
Ile	Arg	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Asn	Ser	Phe	Trp	Ser	Glu
305					310					315					320
Trp	Ala	Ser	Val	Ser	Cys	Ser									
				325											

<210> 29

<211> 984

<212> DNA

<213> Ovis aries

<400> 29

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gctcctggag	aaacagtgg	cctcacgtgt	gacactcctg	aagaagacgg	catcacctgg	180
acctcagacc	agagcagtga	ggtcctgggc	tctggcaaaa	ccttgaccat	ccaagtcaaa	240
gagtttgag	atgctgggca	gtacacctgt	cacaaaaggag	gcgagggttct	gagtcgttca	300
ctcctcctgc	tgcacaaaaa	ggaagatgga	atttgggtcca	ctgatatttt	aaaggatcag	360
aaagaaccca	aagctaagag	ttttttaaaa	tgtgaggcaa	aggattattc	tggaacttc	420
acctgctcgt	ggctgacagc	aatcagtact	aatctgaaat	tcagtgtcaa	aagcagcaga	480
ggctcctctg	acccccgagg	ggtgacgtgc	ggagcagcgt	ccctctcagc	agagaagggtc	540
agcatggacc	acaggggagta	taacaagtac	acagtggagt	gtcaggagg	cagtgcctgc	600
ccggccgccc	aggagagcct	gcccattgag	gtcgtgatgg	aagctgtgca	caagctcaag	660
tatgaaaact	acaccagcag	cttcttcac	aggacatca	tcaaaccaga	cccacccaag	720
aacctgcaac	tgagaccact	aaagaattct	cggcaggtgg	aagtcagctg	ggagtaccct	780
gacacgtgga	gcacccca	ttcctacttc	tccctgacgt	tttgtgttca	ggtccaggga	840

aagaacaaga gagaaaagaa actcttcaca gaccaaact cagccaaagt cacatgccac	900
aaggatgccca acatccgcgt gcaagcccgg gaccgctact acagctcatt ctggagtga	960
tgggcatctg tgcctgcag ttag	984

<210> 30
 <211> 327
 <212> PRT
 <213> Ovis aries

<400> 30

Met	His	Pro	Gln	Gln	Leu	Val	Val	Ser	Trp	Phe	Ser	Leu	Val	Leu	Leu
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Ala	Ser	Pro	Ile	Val	Ala	Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val
			20					25					30		
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asn	Ala	Pro	Gly	Glu	Thr	Val	Val	Leu
			35				40					45			
Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Ser	Asp	Gln
	50					55					60				
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65				70						75				80	
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
				85					90					95	
Leu	Ser	Arg	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Ala	Lys	Ser	Phe
		115					120					125			
Leu	Lys	Cys	Glu	Ala	Lys	Asp	Tyr	Ser	Gly	His	Phe	Thr	Cys	Ser	Trp
	130					135					140				
Leu	Thr	Ala	Ile	Ser	Thr	Asn	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg
145					150					155					160
Gly	Ser	Ser	Asp	Pro	Arg	Gly	Val	Thr	Cys	Gly	Ala	Ala	Ser	Leu	Ser
				165					170					175	
Ala	Glu	Lys	Val	Ser	Met	Asp	His	Arg	Glu	Tyr	Asn	Lys	Tyr	Thr	Val
			180					185					190		
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro
	195						200					205			
Ile	Glu	Val	Val	Met	Glu	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr
	210					215						220			
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys
225					230					235					240
Asn	Leu	Gln	Leu	Arg	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser
				245					250					255	
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu
			260					265					270		
Thr	Phe	Cys	Val	Gln	Val	Gln	Gly	Lys	Asn	Lys	Arg	Glu	Lys	Lys	Leu
		275					280					285			
Phe	Thr	Asp	Gln	Thr	Ser	Ala	Lys	Val	Thr	Cys	His	Lys	Asp	Ala	Asn
	290					295					300				
Ile	Arg	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Phe	Trp	Ser	Glu
305					310					315					320
Trp	Ala	Ser	Val	Ser	Cys	Ser									
				325											

<210> 31
 <211> 1015
 <212> DNA
 <213> Canis familiaris

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<400> 31
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gcccccgag  aaatggtggt cctcacctgc cataccctg aagaagatga catcacttgg      180
acctcagcgc  agagcagtga agtcctaggt tctggtaaaa ctctgaccat ccaagtcaaa      240
gaatttggag  atgctggcca gtatacctgc cataaaggag gcaaggttct gagccgctca      300
ctcctgttga  ttcacaaaaa agaagatgga atttgggtcca ctgatatctt aaaggaacag      360
aaagaatcca  aaaataagat ctttctgaaa tgtgaggcaa agaattattc tggacgtttc      420
acatgctggt  ggctgacggc aatcagtact gatttgaaat tcagtgtcaa aagtagcaga      480
ggcttctctg  accccaaggg ggtgacatgt ggagcagtga cactttcagc agagaggggtc      540
agagtggaca  acagggatta taagaagtac acagtggagt gtcaggaagg cagtgcctgc      600
ccctctgccg  aggagagcct acccatcgag gtcgtggtgg atgctattca caagctcaag      660
tatgaaaact  acaccagcag cttcttcatc agagacatca tcaaaccaga cccaccaca      720
aacctgcagc  tgaagccatt gaaaaattct cggcacgtgg aggtcagctg ggaatacccc      780
gacacctgga  gcacccaca ttcctacttc tccctgacat ttgctgata ggcccagggc      840
aagaacaata  gagaaaagaa agatagactc tgcgtggaca agacctcagc caaggtcgtg      900
tgccacaagg  atgccaagat ccgctgcaa gcccagacc gctactatag ttcacccctg      960
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<210> 32

<211> 329

<212> PRT

<213> Canis familiaris

<400> 32

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Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
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Ala Ser Ser Leu Met Thr Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
 20          25          30
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35          40          45
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
 50          55          60
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65          70          75          80
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
 85          90          95
Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100          105          110
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115          120          125
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130          135          140
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
 145          150          155          160
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
 165          170          175
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180          185          190
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
 195          200          205
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210          215          220
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
 225          230          235          240
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser

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				245					250					255			
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu		
			260					265					270				
Thr	Phe	Cys	Val	Gln	Ala	Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp		
		275					280					285					
Arg	Leu	Cys	Val	Asp	Lys	Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp		
	290					295					300						
Ala	Lys	Ile	Arg	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp		
305				310					315						320		
Ser	Asp	Trp	Ala	Ser	Val	Ser	Cys	Ser									
				325													

<210> 33
 <211> 1005
 <212> DNA
 <213> Cercocebus torquatus

<400> 33
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 acccgatgc ccctggagaa atgggtgggtc tcacctgtga caccctgaa gaagatggta 180
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 gccattcact cctgctgcct cacaaaaagg aagatggaat ttggtccact gatatttta 360
 aggaccagaa agaaccctaaa aatgagacct ttctaagatg cgaggccaaa aattattctg 420
 gacgtatcac ctgctgggtg ctgtcgacaa tcagtactga tctgacattc agtatcataa 480
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 cctgcccagc cgctgaggag aggctgccc ttgaggtcat ggtggatgcc attcacaagc 660
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 accctgacac ctggagtact ccacattcct acttctccct gacattctgc attcaggtcc 840
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<210> 34
 <211> 328
 <212> PRT
 <213> Cercocebus torquatus

<400> 34
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 20 25 30
 Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45
 Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln
 50 55 60
 Ser Gly Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Ala
 85 90 95
 Leu Ser His Ser Leu Leu Leu Pro His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Glu Thr Phe

115	120	125
Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Ile Thr Cys Trp Trp		
130	135	140
Leu Ser Thr Ile Ser Thr Asp Leu Thr Phe Ser Ile Ile Ser Ser Arg		
145	150	155
Gly Ser Ser Asn Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser		
165	170	175
Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu		
180	185	190
Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Arg Leu Pro Ile		
195	200	205
Glu Val Met Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr		
210	215	220
Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn		
225	230	235
Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp		
245	250	255
Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr		
260	265	270
Phe Cys Ile Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg		
275	280	285
Ile Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala		
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305	310	315
Glu Trp Thr Ser Val Pro Cys Ser		
325		

<210> 35

<211> 984

<212> DNA

<213> Marmota monax

<400> 35

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acacctggag	aaaaggtggt	cctcacctgt	gacactcctg	aagaagacgg	catcacctgg	180
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gagtttgaag	acgctggcca	ctacacctgc	cgcagaggag	gtgaagttct	gagccagatg	300
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gaacctgaaa	ataagaacct	tgaacatgc	gaggcaaaga	attactctgg	acgttttacc	420
tgctggtggc	tgacggcaat	cagtactgat	gtgaacttca	gtgtcaagag	ccacagaggc	480
tcctctgacc	ctcaaggggt	gacgtgtgga	gaagcaactc	tctctgcaga	gaggggtcaa	540
atagagcaga	gggagtacaa	gaagtactcg	gtgcagtgcc	aggaggacaa	tgcctgcccc	600
accgctgagg	agaccctgcc	catcacagtg	gtggtggacg	cagttcacia	gctcaagtac	660
gaaaactaca	tcagcagctt	cttcacacaga	gacatcatca	aacctgaccc	acccaagaac	720
ctaaagatga	agccatccaa	gactcctcag	caggtggagg	tcacctggga	gtacccggac	780
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aagaagaaaa	ggagcaatac	tctccacgtg	gataagacct	cagtcacagt	gacctgccag	900
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<210> 36

<211> 327

<212> PRT

<213> Marmota monax

Met 1	Cys	Leu	Gln	Gln	Leu	Val	Ile	Ser	Trp	Val	Ser	Leu	Val	Trp	Leu
Ala	Ser	Pro	Leu	Leu	Ala	Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val
Val	Glu	Leu	Asp	Trp	His	Pro	Asp	Thr	Pro	Gly	Glu	Lys	Val	Val	Leu
Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Ser	Glu	Gln
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Leu	Val	Lys
65	Glu	Phe	Glu	Asp	Ala	Gly	His	Tyr	Thr	Cys	Arg	Arg	Gly	Gly	Glu
Leu	Ser	Gln	Met	Leu	Leu	Leu	Leu	His	Lys	Asn	Glu	Asp	Gly	Ile	Trp
Ser	Thr	Asp	Ile	Leu	Lys	Lys	Lys	Glu	Pro	Glu	Asn	Lys	Asn	Leu	Val
Thr	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu
Thr	Ala	Ile	Ser	Thr	Asp	Val	Asn	Phe	Ser	Val	Lys	Ser	His	Arg	Gly
145	Ser	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Glu	Ala	Thr	Leu	Ser
Glu	Arg	Val	Lys	Ile	Glu	Gln	Arg	Glu	Tyr	Lys	Lys	Tyr	Ser	Val	Gln
Cys	Gln	Glu	Asp	Asn	Ala	Cys	Pro	Thr	Ala	Glu	Glu	Thr	Leu	Pro	Ile
Thr	Val	Val	Val	Asp	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Ile
Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn
225	Leu	Lys	Met	Lys	Pro	Ser	Lys	Thr	Pro	Gln	Gln	Val	Glu	Val	Thr
Glu	Tyr	Pro	Asp	Ser	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr
Phe	Ser	Val	Gln	Val	Gln	Gly	Lys	Lys	Lys	Lys	Arg	Ser	Asn	Thr	Leu
His	Val	Asp	Lys	Thr	Ser	Val	Thr	Val	Thr	Cys	Gln	Lys	Gly	Ala	Lys
Val	Ser	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Asn	Ser	Ser	Trp	Ser	Glu
305	Trp	Ala	Thr	Met	Ser	Cys	Pro								